

Db 64 MTDYLLNLALSDLEFFLTPFWAHYAAGQWDFGNTMCQFLTGLYFIFGFSGIFILLT 123
 QY 136 IDRYLAIVHAFALKARTVFGVTSVITLWVAFASVPGIIFTKCQKEDSVYVCGPYPP 195
 Db 124 IDRYLAIVHAFALKARTVFGVTSVITWVAFASVPGIIFTRSQEGYHYTCSPPFP 183
 QY 196 RG----WNNPHTIMRNILGLVPLLMVICYSGLIKTLRLCRNEKKRRHRAVRVITMIV 251
 Db 184 FGVRFWKLETLKMWILGLVPLLMVICYSGLIKTLRLCRNEKKRRHRAVRVITMIV 243
 QY 252 YFLFWPYNIVILLNTQEFFGLSNCESTSQLDOATQVTEFLGTHCCINPIIYAFVGEK 311
 Db 244 YFLFWPYNIVILLNTQEFFGLSNCESTSQLDOATQVTEFLGTHCCINPIIYAFVGEK 303
 QY 312 FRSLF-----HIA 319
 Db 304 FRNLLVFFQKHIA 317

RESULT 2

Q9TUV8 PRELIMINARY; PRT; 339 AA.
 AC Q9TUV8
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 GN CCR5.
 OS Saguinus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
 OX NCBI_TaxID=100754;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161929; AAD47686.1; -
 DR InterPro; IPR000923; BlueCu_1.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_Rhodpsn.
 DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 FT NON_TER
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 339 AA; 39164 MW; 6A67CF5D22C70C49 CRC64;

Query Match 63.1%; Score 1244; DB 6; Length 339;
 Best Local Similarity 77.3%; Pred. No. 7.3e-102;
 Matches 238; Conservative 24; Mismatches 34; Indels 12; Gaps 3;

QY 24 FDYDYG--APCHKFDVKQIGQAQLLPPLYSLVIFGFGVGNMVLVILINCKKLCITDIYL 81
 Db 3 YDIDYGPSEPKRIDVKQMGHALLPPLYSWVLFEGVGNMVLVILINCKRKSMTDIYL 62
 QY 82 LNLALSLLFLITLPLWAHSAANWVFGNACKLFTGLYHIGVFGGIFILLTIDRYLA 141
 Db 63 LNLALSLLFLITVFWAHYAAGQWDFGNTMCQFLTGLYFIFGFSGIFILLTIDRYLA 122
 QY 142 IVHAFALKARTVFGVTSVITLWVAFASVPGIIFTKCQKEDSVYVCGPYPPG--- 197
 Db 123 IVHAFALKARTVFGVTSVITLWVAFASVPGIIFTRSQEGYHYTCSPPFPQYOF 182
 QY 198 WNNPHTIMRNILGLVPLLMVICYSGLIKTLRLCRNEKKRRHRAVRVITMIVFLFWT 257
 Db 183 WKNFETLKMVLGLVPLLMVICYSGLIKTLRLCRNEKKRRHRAVRVITMIVFLFWA 242

QY 258 PYNIVILLNTQEFFGLSNCESTSQLDOATQVTEFLGTHCCINPIIYAFVGEKFRSLF- 316
 Db 243 PYNIVILLNTQEFFGLSNCESTSQLDOATQVTEFLGTHCCINPIIYAFVGEKFRNLY 302
 QY 317 -----HIA 319
 Db 303 VFFQKHIA 310

RESULT 3

Q9TOT3 PRELIMINARY; PRT; 339 AA.
 AC Q9TOT3
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 GN CCR5.
 OS Callithrix jacchus (Common marmoset).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
 OX NCBI_TaxID=9483;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF162021; AAD47776.1; -
 DR EMBL; AF161934; AAD47691.1; -
 DR EMBL; AF161935; AAD47692.1; -
 DR EMBL; AF161936; AAD47693.1; -
 DR EMBL; AF161937; AAD47694.1; -
 DR EMBL; AF161938; AAD47695.1; -
 DR EMBL; AF161939; AAD47696.1; -
 DR EMBL; AF161940; AAD47697.1; -
 DR EMBL; AF161944; AAD47700.1; -
 DR InterPro; IPR000923; BlueCu_1.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_Rhodpsn.
 DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 FT NON_TER
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 339 AA; 39055 MW; C1313952E71B50C7 CRC64;

Query Match 63.1%; Score 1244; DB 6; Length 339;
 Best Local Similarity 76.6%; Pred. No. 7.3e-102;
 Matches 236; Conservative 27; Mismatches 33; Indels 12; Gaps 3;

QY 24 FDYDYG--APCHKFDVKQIGQAQLLPPLYSLVIFGFGVGNMVLVILINCKKLCITDIYL 81
 Db 3 YDIDYGPSEPKRIDVKQMGHALLPPLYSWVLFEGVGNMVLVILINCKRKSMTDIYL 62
 QY 82 LNLALSLLFLITLPLWAHSAANWVFGNACKLFTGLYHIGVFGGIFILLTIDRYLA 141
 Db 63 LNLALSLLFLITVFWAHYAAGQWDFGNTMCQFLTGLYFIFGFSGIFILLTIDRYLA 122
 QY 142 IVHAFALKARTVFGVTSVITLWVAFASVPGIIFTKCQKEDSVYVCGPYPP--- 197
 Db 123 IVHAFALKARTVFGVTSVITLWVAFASVPGIIFTRSQEGYHYTCSPPFPQYOF 182
 QY 198 WNNPHTIMRNILGLVPLLMVICYSGLIKTLRLCRNEKKRRHRAVRVITMIVFLFWT 257
 Db 183 WKNFETLKMVLGLVPLLMVICYSGLIKTLRLCRNEKKRRHRAVRVITMIVFLFWA 242
 QY 258 PYNIVILLNTQEFFGLSNCESTSQLDOATQVTEFLGTHCCINPIIYAFVGEKFRSLF- 316
 Db 243 PYNIVILLNTQEFFGLSNCESTSQLDOATQVTEFLGTHCCINPNPIIYAFVGEKFRNLY 302

QY 317 -----HIA 319
 Db 303 VFFQKHIA 310

RESULT 4

Q9MZA0 PRELIMINARY; PRT; 352 AA.
 AC Q9MZA0;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE CC chemokine receptor 5 (C-C chemokine receptor 5).
 GN CCR5.
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
 OX NCBI_TaxID=9483;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20317091; PubMed=10747879;
 RX Mummidi S., Banshad M., Ahuja S.S., Gonzalez E., Feuillet P.M.,
 RA Begum K., Galvis M.C., Kosteki V., Valente A.J., Murthy K.K.,
 RA Haro L., Dolan M.J., Allan J.S., Ahuja S.K.;
 RA "Evolution of human and non-human primate CC chemokine receptor 5 gene
 RT and mRNA. Potential roles for haplotype and mRNA diversity,
 RT differential haplotype-specific transcriptional activity, and altered
 RT transcription factor binding to polymorphic nucleotides in the
 RT pathogenesis of HIV-1 and simian immunodeficiency virus.";
 RL J. Biol. Chem. 275:18946-18961(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Zhang Y., Ryder O.A., Zhang Y.;
 RA "Sequence comparison of the CCR5 gene in primates and primate
 RT phylogeny.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF252554; AAF87984.1; -
 DR EMBL: AF177878; AAK43361.1; -
 DR InterPro: IPR000923; BlueCu1.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00196; COPPER_HODOPSIN.
 DR PROSITE: PS00237; G_PROTEIN_RECF_1; UNKNOWN_1.
 DR PROSITE: PS00262; G_PROTEIN_RECF_2; 1.
 KW Receptor.
 SQ SEQUENCE 352 AA; 40465 MW; FF0D0A8D06F7B8F5 CRC64;
 Query Match 63.1%; Score 1244; DB 6; Length 352;
 Best Local Similarity 76.6%; Pred. No. 7.5e-102;
 Matches 236; Conservative 27; Mismatches 33; Indels 12; Gaps 3;
 QY 24 FDYDG--APCHKFDVKQIGAQLLPPLYSLVFIFGVGNMVLVLLINCKKLCITDIYL 81
 Db 10 YDIDYGPSEPCRKIDVKQGAHLLPPLYSMLVFLGVGNMVLVLLINCKKLSMTDIYL 69
 QY 82 LNLATSDLLFLITPLWAHSAANEVFGNACKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
 Db 70 LNLATSDLLFLITPLWAHSAANEVFGNACKLFTGLYHIGYFGGIFFIILLTIDRYLA 129
 QY 142 IVHAVFALKARTVFGVTSVITLWVAVFASVPGIIFTKCKEDSVVYCGVPYPRG---RG 197
 Db 130 IVHAVFALKARTVFGVTSVITLWVAVFASVPGIIFTKCKEDSVVYCGVPYPRG---RG 189
 QY 198 WNNFHTIMRNILGLVPLLMVICYSGILKTLRLCRNEKKRRHRAVFIIMVYFLFWT 257
 Db 190 WNNFHTIMRNILGLVPLLMVICYSGILKTLRLCRNEKKRRHRAVFIIMVYFLFWA 249
 QY 258 PYNIVILLNTFOEFFGLSNCESTSLDQATQVTEITLGMTHCCINPIIYAFVGEKFRSLF- 316
 Db 250 PYNIVILLNTFOEFFGLSNCESTSLDQATQVTEITLGMTHCCINPIIYAFVGEKFRSLF- 309

QY 317 -----HIA 319
 Db 310 VFFQKHIA 317

RESULT 5

Q9TQV5 PRELIMINARY; PRT; 339 AA.
 AC Q9TQV5; 2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 GN CCR5.
 OS Saginus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saginus.
 OX NCBI_TaxID=100754;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Oprende J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RA "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF161931; AAD47688.1; -
 DR EMBL: AF161923; AAD47680.1; -
 DR EMBL: AF161925; AAD47682.1; -
 DR EMBL: AF161926; AAD47683.1; -
 DR InterPro: IPR000923; BlueCu1.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00196; COPPER_HODOPSIN.
 DR PROSITE: PS00237; G_PROTEIN_RECF_1; UNKNOWN_1.
 DR PROSITE: PS00262; G_PROTEIN_RECF_2; 1.
 KW Receptor.
 FT NON_TER 1 1
 FT NON_TER 339 339
 SQ SEQUENCE 339 AA; 39081 MW; 6B79D05D22C70032 CRC64;
 Query Match 63.1%; Score 1243; DB 6; Length 339;
 Best Local Similarity 76.9%; Pred. No. 8.9e-102;
 Matches 237; Conservative 25; Mismatches 34; Indels 12; Gaps 3;
 QY 24 FDYDG--APCHKFDVKQIGAQLLPPLYSLVFIFGVGNMVLVLLINCKKLCITDIYL 81
 Db 3 YDIDYGPSEPCRKIDVKQGAHLLPPLYSMLVFLGVGNMVLVLLINCKKPSMTDIYL 62
 QY 82 LNLATSDLLFLITPLWAHSAANEVFGNACKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
 Db 63 LNLATSDLLFLITPLWAHSAANEVFGNACKLFTGLYHIGYFGGIFFIILLTIDRYLA 122
 QY 142 IVHAVFALKARTVFGVTSVITLWVAVFASVPGIIFTKCKEDSVVYCGVPYPRG--- 197
 Db 123 IVHAVFALKARTVFGVTSVITLWVAVFASVPGIIFTKCKEDSVVYCGVPYPRG--- 182
 QY 198 WNNFHTIMRNILGLVPLLMVICYSGILKTLRLCRNEKKRRHRAVFIIMVYFLFWT 257
 Db 183 WNNFHTIMRNILGLVPLLMVICYSGILKTLRLCRNEKKRRHRAVFIIMVYFLFWA 242
 QY 258 PYNIVILLNTFOEFFGLSNCESTSLDQATQVTEITLGMTHCCINPIIYAFVGEKFRSLF- 316
 Db 243 PYNIVILLNTFOEFFGLSNCESTSLDQATQVTEITLGMTHCCINPIIYAFVGEKFRSLF- 302
 QY 317 -----HIA 319
 Db 303 VFFQKHIA 310

RESULT 6

Q95NC4 PRELIMINARY; PRT; 352 AA.
 ID Q95NC4

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AC Q95NC4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE C-C chemokine receptor 5.
GN CCR5.
OS Ateles geoffroyi (Black-handed spider monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Ateleinae; Ateles.
OX NCBI_TaxID=9509;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Ryder O.A., Zhang Y.;
RT "Sequence comparison of the CCR5 gene in primates and primate
RT phylogeny.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AFI17785; AAK43368.1; -.
DR InterPro; IPR000923; BlueCu_1.
DR InterPro; IPR000276; GPCR_Rhodpsn.
GN pfam: PF00001; 7tm.1; 1.
OS PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
OS PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 352 AA; 40440 MW; F0A686CB4FE3964B CRC64;

Query Match 63.1%; Score 1243; DB 6; Length 352;
Best Local Similarity 76.6%; Pred. No. 9.2e-102;
Matches 236; Conservative 27; Mismatches 33; Indels 12; Gaps 3;

QY 24 FDYDYG--PCHKFDVKQIGALLPPLYSIVFIFGVGNMVLVILINCKKLCITDIYL 81
DB 10 YDIDYGSEPCRKIDVKQGAHLLPPLYSIVFIFGVGNMVLVILINCKRPSMTDIYL 69
QY 82 LNLAISSLFLITLPLWAHSAANEVFGNACMLKFTGLYHIGYFGGIFILLTIDRYLA 141
DB 70 LNLAISSLFLITLPLWAHSAANEVFGNACMLKFTGLYHIGYFGGIFILLTIDRYLA 129
QY 142 IVHAVFALKARTVFGVTVSVITWLVAVFASVPGIIFTKCKEDSVYVCGPYFPRG---- 197
DB 130 IVHAVFALKARTVFGVTVSVITWLVAVFASVPGIIFTKCKEDSVYVCGPYFPRG 189
QY 198 WNNFHTIMRNILGLVPLLMIVICYSGLIKTLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
DB 190 WKNFETLKMVILGLVPLLMIVICYSGLIKTLRCRNEKKRHRAVRVIFTIMIVYFLFWA 249
QY 258 PYNIVILLNTQEPFGLSNCESTSQLDQATQVETLGMTHCCINPIIYAFVGEKFRSLF- 316
DB 250 PYNIVILLNTQEPFGLSNCESTSQLDQATQVETLGMTHCCINPIIYAFVGEKFRNLL 309
QY 317 -----HIA 319
DB 310 VFFQKHIA 317

RESULT 7
Q9TUW0 PRELIMINARY; PRT; 339 AA.
AC Q9TUW0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Saguinus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX NCBI_TaxID=100754;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
```

```
RT species ";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AFI161927; AAD47684.1; -.
DR InterPro; IPR000923; BlueCu_1.
DR InterPro; IPR000276; GPCR_Rhodpsn.
GN pfam: PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPS.
DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 339
SQ SEQUENCE 339 AA; 39065 MW; 7B358C51728B5C32 CRC64;

Query Match 62.9%; Score 1240; DB 6; Length 339;
Best Local Similarity 76.9%; Pred. No. 1.6e-101;
Matches 237; Conservative 24; Mismatches 35; Indels 12; Gaps 3;

QY 24 FDYDYG--APCHKFDVKQIGALLPPLYSIVFIFGVGNMVLVILINCKKLCITDIYL 81
DB 3 YDIDYGSEPCRKIDVKQGAHLLPPLYSIVFIFGVGNMVLVILINCKRPSMTDIYL 62
QY 82 LNLAISSLFLITLPLWAHSAANEVFGNACMLKFTGLYHIGYFGGIFILLTIDRYLA 141
DB 63 LNLAISSLFLITLPLWAHSAANEVFGNACMLKFTGLYHIGYFGGIFILLTIDRYLA 122
QY 142 IVHAVFALKARTVFGVTVSVITWLVAVFASVPGIIFTKCKEDSVYVCGPYFPRG---- 197
DB 123 IVHAVFALKARTVFGVTVSVITWLVAVFASVPGIIFTKCKEDSVYVCGPYFPRG 182
QY 198 WNNFHTIMRNILGLVPLLMIVICYSGLIKTLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
DB 183 WKNFETLKMVILGLVPLLMIVICYSGLIKTLRCRNEKKRHRAVRVIFTIMIVYFLFWA 242
QY 258 PYNIVILLNTQEPFGLSNCESTSQLDQATQVETLGMTHCCINPIIYAFVGEKFRSLF- 316
DB 243 PYNIVILLNTQEPFGLSNCESTSQLDQATQVETLGMTHCCINPIIYAFVGEKFRNLL 302
QY 317 -----HIA 319
DB 303 VFFQKHIA 310

RESULT 8
Q9MZ99 PRELIMINARY; PRT; 352 AA.
AC Q9MZ99;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE CC chemokine receptor 5.
GN CCR5.
OS Ateles sp. (Spider monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Ateleinae; Ateles.
OX NCBI_TaxID=9511;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20317091; PubMed=10747879;
RA Mummidi S., Bamsad M., Ahuja S.S., Gonzalez E., Feuillet P.M.,
RA Begum K., Galvis M.C., Kostecki V., Valente A.J., Murthy K.K.,
RA Haro L., Dolan M.J., Allan J.S., Ahuja S.K.;
RT "Evolution of human and non-human primate CC chemokine receptor 5 gene
RT and mRNA. Potential roles for haplotype and mRNA diversity,
RT differential haplotype-specific transcriptional activity, and altered
RT transcription factor binding to polymorphic nucleotides in the
RT pathogenesis of HIV-1 and simian immunodeficiency virus.";
RL J. Biol. Chem. 275:18946-18961(2000).
DR EMBL; AF252555; AAF87985.1; -.
DR InterPro; IPR000923; BlueCu_1.
DR InterPro; IPR000276; GPCR_Rhodpsn.
GN pfam: PF00001; 7tm.1; 1.
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DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_FL_2; 1.
 KW Receptor.
 SQ SEQUENCE 352 AA; 40471 MW; 01E397C2A87DE64D CRC64;
 Query Match 62.9%; Score 1239; DB 6; Length 352;
 Best Local Similarity 76.3%; Pred. No. 2.1e-101;
 Matches 235; Conservative 27; Mismatches 34; Indels 12; Gaps 3;
 QY 24 FDYDYG--PCCHKEDVKOIGAQQLPPLYSLVFIKFGVGNMVLVLLINCKKLCITDIYL 81
 Db 10 YDIDYGSEPCRKIDVKQMGHLLPPLYSVWFLFVGVGNMVLVLLINCKKPKSMTDIYL 69
 QY 82 LNLAISDLLFLITLPLWAHSAANWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
 Db 70 LNLTSIDLLFLFTVFWAHYAAGQWDFGNTMCQFLTGLYFGGIFFIILLTIDRYLA 129
 QY 142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVYVCGPYFPRG---- 197
 Db 130 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTRSQEGVHYTCSPHFPFGQYOF 189
 QY 198 WNNFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKKRHRVAVRFTIMIVVFLFWT 257
 Db 190 WNFETLKMVILGLVPLLMVICYSGILKTLRCRNEKKRHRVAVRFTIMIVVFLFWA 249
 QY 258 PYNIVILLNTFOEFGLSNCESTSQLDQATQVTEGLMTHCCINPIIYAFVGEKFRSLP- 316
 Db 250 PYNIVILLNTYOEFGGLNCCSSNRLDQAMQVTEGLMTHCCVNPPIIYAFVGEKFRNYLL 309
 QY 317 -----HIA 319
 Db 310 VEFQKHIA 317

RESULT 9
 Q9TUV6 PRELIMINARY; PRT; 339 AA.
 AC Q9TUV6
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 GN CCR5.
 OS Saguinus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
 OX NCBI_TaxID=100754;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species."
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161932; AAD47689.1; -
 DR InterPro; IPR000923; BlueCu.1.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_FL_2; 1.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 339
 SQ SEQUENCE 339 AA; 38993 MW; 0559F4F0FEC70F5F CRC64;
 Query Match 62.9%; Score 1238.5; DB 6; Length 339;
 Best Local Similarity 75.3%; Pred. No. 2.2e-101;
 Matches 236; Conservative 26; Mismatches 43; Indels 9; Gaps 3;

QY 24 FDYDYG--APCHKEDVKOIGAQQLPPLYSLVFIKFGVGNMVLVLLINCKKLCITDIYL 81
 Db 3 YDIDYGSEPCRKIDVKQMGHLLPPLYSVWFLFVGVGNMVLVLLINCKKPKSMTDIYL 62
 QY 82 LNLAISDLLFLITLPLWAHSAANWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
 Db 63 LNLAISDLIFFTVFWAHYAAGQWDFGNTMCQFLTGLYFGGIFFIILLTIDRYLA 122
 QY 142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVYVCGPYFPRG---- 197
 Db 133 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTRSQEGVHYTCSPHFPFGQYOF 182
 QY 198 WNNFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKKRHRVAVRFTIMIVVFLFWT 257
 Db 183 WNFETLKMVILGLVPLLMVICYSGILKTLRCRNEKKRHRVAVRFTIMIVVFLFWA 242
 QY 258 PYNIVILLNTFOEFGLSNCESTSQLDQATQVTEGLMTHCCINPIIYAFVGEKFRSLP 317
 Db 243 PYNIVILLNTYOEFGGLNCCSSNRLDQAMQVTEGLMTHCCVNPPIIYAFVGEKFRNYLV 302
 QY 318 IALGCRPIAPLOKPVCG 333
 Db 303 VEFQKHIA--KFCG 315
 RESULT 10
 Q9TUM1 PRELIMINARY; PRT; 339 AA.
 AC Q9TUM1
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 GN CCR5.
 OS Saguinus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
 OX NCBI_TaxID=100754;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species."
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161924; AAD47681.1; -
 DR InterPro; IPR000923; BlueCu.1.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_FL_2; 1.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 339
 SQ SEQUENCE 339 AA; 39069 MW; 5146237770BC70028 CRC64;
 Query Match 62.8%; Score 1238; DB 6; Length 339;
 Best Local Similarity 76.6%; Pred. No. 2.5e-101;
 Matches 236; Conservative 25; Mismatches 35; Indels 12; Gaps 3;
 QY 24 FDYDYG--APCHKEDVKOIGAQQLPPLYSLVFIKFGVGNMVLVLLINCKKLCITDIYL 81
 Db 3 YDIDYGSEPCRKIDVKQMGHLLPPLYSVWFLFVGVGNMVLVLLINCKKPKSMTDIYL 62
 QY 82 LNLAISDLLFLITLPLWAHSAANWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
 Db 63 LNLAISDLIFFTVFWAHYAAGQWDFGNTMCQFLTGLYFGGIFFIILLTIDRYLA 122
 QY 142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVYVCGPYFPRG---- 197
 Db 123 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTRSQEGVHYTCSPHFPFGQYOF 182

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QY 198 WNNFHTIMRNILGLVPLLMIVICYSGLKTLRCRNEKKRRHRAVRVIFTIMIVYFLWT 257
DB 183 WKNFETLKMVILGLVPLLTVMIVICYSGLKTLRCRNEKKRRHRAVRVIFTIMIVYFLWA 242
QY 258 PYNIVILLNTQEFGLNCSNSTOLDQATQVTEFLGTHCCINPIIYAFVGEKFRSLF- 316
DB 243 PYNIVILLNTQEFGLNCSNSTOLDQAMQVTEFLGTHCCINPIIYAFVGEKFRNLYV 302
QY 317 -----HIA 319
DB 303 VFFQKHIA 310

RESULT 11
Q9TUV9 ID Q9TUV9 PRELIMINARY; PRT; 339 AA.
AC Q9TUV9;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX NCBI_TaxID=100754;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161928; AAD47685.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 66P33F6022C71F0F CRC64;

Query Match 62.8%; Score 1237; DB 6; Length 339;
Best Local Similarity 76.6%; Pred. No. 3e-101;
Matches 236; Conservative 25; Mismatches 35; Indels 12; Gaps 3;

QY 24 FDYDYG--APCHKFDVKQIGAOQLPPLYSILVTFGFGVGNMVLVILINCKLKCLTDIYL 81
DB 3 YDIDYGSPCKRIDVKQGAHLPLPLYSILVTFGFGVGNMVLVILINCKLKCLTDIYL 62
QY 82 LNAISDLFLTLPLWAHSAANEWFGNAMKLTGLYHIGYFGGFIITLLTDIYLA 141
DB 63 LNAISDLFLTLVPEWHAHAAQWDFGNTMCQFLTGLYFGGFIITLLTDIYLA 122
QY 142 IVHAVFALKARTVTFGVTSVITLWVAVFASVPGIIFTKCKEDSVYVCGPYPRG---- 197
DB 123 IVHAVFALKARTVTFGVTSVITLWVAVFASVPGIIFTKCKEDSVYVCGPYPRG 182
QY 198 WNNFHTIMRNILGLVPLLMIVICYSGLKTLRCRNEKKRRHRAVRVIFTIMIVYFLWT 257
DB 183 WKNFETLKMVILGLVPLLTVMIVICYSGLKTLRCRNEKKRRHRAVRVIFTIMIVYFLWA 242
QY 258 PYNIVILLNTQEFGLNCSNSTOLDQATQVTEFLGTHCCINPIIYAFVGEKFRSLF- 316
DB 243 PYNIVILLNTQEFGLNCSNSTOLDQAMQVTEFLGTHCCINPIIYAFVGEKFRNLYV 302
QY 317 -----HIA 319
DB 303 VFFQKHIA 310

RESULT 12
Q9TOWO ID Q9TOWO PRELIMINARY; PRT; 339 AA.
AC Q9TOWO;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162024; AAD47779.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 5555FEAF2614D35C CRC64;

Query Match 62.7%; Score 1236; DB 6; Length 339;
Best Local Similarity 77.4%; Pred. No. 3.7e-101;
Matches 236; Conservative 25; Mismatches 34; Indels 10; Gaps 2;

QY 25 DYDYGAPCHKFDVKQIGAOQLPPLYSILVTFGFGVGNMVLVILINCKLKCLTDIYLLN 84
DB 6 DYTSEPCQKINVKQIAARLLPPLYSILVTFGFGVGNMVLVILINCKLKCLTDIYLLN 65
QY 85 AISDLLFLTLPLWAHSAANEWFGNAMKLTGLYHIGYFGGFIITLLTDIYLAIVH 144
DB 66 AISDLFLTLVPEWHAHAAQWDFGNTMCQFLTGLYFGGFIITLLTDIYLAIVH 125
QY 145 AVFALKARTVTFGVTSVITLWVAVFASVPGIIFTKCKEDSVYVCGPYPRF---RGWNN 200
DB 126 AVFALKARTVTFGVTSVITLWVAVFASVPGIIFTKCKEDSVYVCGPYPRF 185
QY 201 FHTIMRNILGLVPLLMIVICYSGLKTLRCRNEKKRRHRAVRVIFTIMIVYFLWT 260
DB 186 FQTLKIVILGLVPLLMIVICYSGLKTLRCRNEKKRRHRAVRVIFTIMIVYFLWAPYN 245
QY 261 IVLLNTQEFGLNCSNSTOLDQATQVTEFLGTHCCINPIIYAFVGEKFRSLF---- 316
DB 246 IVLLNTQEFGLNCSNSTOLDQAMQVTEFLGTHCCINPIIYAFVGEKFRNLYV 305
QY 317 --HIA 319
DB 306 QKHIA 310

RESULT 13
Q9TSN3 ID Q9TSN3 PRELIMINARY; PRT; 339 AA.
AC Q9TSN3;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.

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OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161951; AAD47707.1; -;
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCRHHODOPS.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON_TER 1 339
 FT NON_TER 339 339
 SQ SEQUENCE 339 AA; 3908 MW; F0132E8BC44EFB29 CRC64;
 Query Match 62.7%; Score 1235; DB 6; Length 339;
 Best Local Similarity 77.3%; Pred. No. 4.5e-101;
 Matches 238; Conservative 25; Mismatches 33; Indels 12; Gaps 3;
 QY 24 FDYDYG--GAPCHFDVQKQIAQLLPPLYSILVIFGFGVGNMLVLLINCKLKCLTDIYL 81
 Db 3 YDIYITSEPCQKINVKQIAARLLPPLYSILVIFGFGVGNMLVLLINCKLKCLTDIYL 62
 QY 82 LNLAISDLLEFLITLPLWAHSAANEVFGNAMCKLTGLYHIGYFGGFIFFILLTIDRYLA 141
 Db 63 LNLAISDLLEFLITLPLWAHSAANEVFGNAMCKLTGLYHIGYFGGFIFFILLTIDRYLA 122
 QY 142 IVHAFVFAKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVVCGPYFP---RG 197
 Db 123 IVHAFVFAKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVVCGPYFP---RG 182
 QY 198 WNNPHTTMRNLGLVPLLMVICYSGILTKLLRCRNEKKRHRVAVFTIMIVYFLFWT 257
 Db 183 WNNPHTTMRNLGLVPLLMVICYSGILTKLLRCRNEKKRHRVAVFTIMIVYFLFWT 242
 QY 258 PYNIVLLNTFOEFGFLSNCESTSQLDQATQVETLGMTHCCINPIIYAFVGEKFRSLF- 316
 Db 243 PYNIVLLNTFOEFGFLSNCESTSQLDQATQVETLGMTHCCINPIIYAFVGEKFRSLF- 302
 QY 317 -----HIA 319
 Db 303 VFFQKHIA 310
 RESULT 14
 O77776
 ID O77776 PRELIMINARY; PRT; 352 AA.
 AC O77776;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE C-C chemokine receptor CCR5.
 GN CCR5.
 OS Cercocebus torquatus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Cercocebus.
 OX NCBI_TaxID=81944;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1208;
 RA Chen Z., Kwon D., Jin Z., Monard S., Telfer P., Jones M., Lu C.,
 RA Aguilar R., Ho D.D., Marx P.A.;
 RT "Natural infection of a homozygous delta 24 CCR5 red-capped mangabey
 with a R2b-tropic simian immunodeficiency virus.";

J. Exp. Med. 0:0-0(1998).
 EMBL; AF084004; AAC62472.1; -;
 InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCRHHODOPS.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 352 AA; 40475 MW; B3A63FDC4473DID3 CRC64;
 Query Match 62.7%; Score 1235; DB 6; Length 352;
 Best Local Similarity 76.9%; Pred. No. 4.7e-101;
 Matches 237; Conservative 27; Mismatches 32; Indels 12; Gaps 3;
 QY 24 FDYDYG--GAPCHFDVQKQIAQLLPPLYSILVIFGFGVGNMLVLLINCKLKCLTDIYL 81
 Db 10 YDIYITSEPCQKINVKQIAARLLPPLYSILVIFGFGVGNMLVLLINCKLKCLTDIYL 69
 QY 82 LNLAISDLLEFLITLPLWAHSAANEVFGNAMCKLTGLYHIGYFGGFIFFILLTIDRYLA 141
 Db 70 LNLAISDLLEFLITLPLWAHSAANEVFGNAMCKLTGLYHIGYFGGFIFFILLTIDRYLA 129
 QY 142 IVHAFVFAKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVVCGPYFP---RG 197
 Db 130 IVHAFVFAKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVVCGPYFP---RG 189
 QY 198 WNNPHTTMRNLGLVPLLMVICYSGILTKLLRCRNEKKRHRVAVFTIMIVYFLFWT 257
 Db 190 WNNPHTTMRNLGLVPLLMVICYSGILTKLLRCRNEKKRHRVAVFTIMIVYFLFWT 249
 QY 258 PYNIVLLNTFOEFGFLSNCESTSQLDQATQVETLGMTHCCINPIIYAFVGEKFRSLF- 316
 Db 250 PYNIVLLNTFOEFGFLSNCESTSQLDQATQVETLGMTHCCINPIIYAFVGEKFRSLF- 309
 QY 317 -----HIA 319
 Db 310 VFFQKHIA 317
 RESULT 15
 O9TUV5
 ID O9TUV5 PRELIMINARY; PRT; 339 AA.
 AC O9TUV5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20; Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 GN CCR5.
 OS Saguinus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
 OX NCBI_TaxID=100754;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161933; AAD47690.1; -;
 DR InterPro; IPR000923; BlueCu1.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCRHHODOPS.
 DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON_TER 1 339
 FT NON_TER 339 339
 SQ SEQUENCE 339 AA; 39021 MW; 8DACBD0D6C785073 CRC64;
 Query Match 62.6%; Score 1234; DB 6; Length 339;

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